PCT09

RAW SEQUENCE LISTING   DATE: 11/14/2001
PATENT APPLICATION: US/09/743,823   TIME: 14:15:45

Input Set : A:\6184844j.app
Output Set: N:\CRF3\11142001\I743823.raw

```
 3 <110> APPLICANT: FOGHER, CORRADO
 5 <120> TITLE OF INVENTION: A SYNTHETIC POLYNUCLEOTIDE CODING FOR HUMAN
 6       LACTOFERRIN, VECTORS, CELLS AND TRANSGENIC PLANTS
 7       CONTAINING IT
 9 <130> FILE REFERENCE: 618484-4/JP/B-4075PCT
11 <140> CURRENT APPLICATION NUMBER: 09/743,823
12 <141> CURRENT FILING DATE: 2001-01-16
14 <150> PRIOR APPLICATION NUMBER: IT RM98A000478
15 <151> PRIOR FILING DATE: 1998-07-17
17 <160> NUMBER OF SEQ ID NOS: 25
19 <170> SOFTWARE: PatentIn Ver. 2.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 2079
23 <212> TYPE: DNA
24 <213> ORGANISM: Artificial Sequence
26 <220> FEATURE:
27 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
28       encoding human lactoferrin
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (1)..(2076)
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35 ggc cgt agg aga agg agt gtt caa tgg tgc gca gta tca caa cca gag    48
36 Gly Arg Arg Arg Arg Ser Val Gln Trp Cys Ala Val Ser Gln Pro Glu
37  1               5                   10                  15
39 gcc aca aaa tgc ttc caa tgg caa agg aat atg aga aaa gtt cgt gga    96
40 Ala Thr Lys Cys Phe Gln Trp Gln Arg Asn Met Arg Lys Val Arg Gly
41              20                  25                  30
43 cct cct gta tct tgc ata aag aga gat tca ccc atc cag tgt atc cag   144
44 Pro Pro Val Ser Cys Ile Lys Arg Asp Ser Pro Ile Gln Cys Ile Gln
45          35                  40                  45
47 gca att gcg gaa aac aga gct gat gct gtg act ctt gat ggt ggt ttc   192
48 Ala Ile Ala Glu Asn Arg Ala Asp Ala Val Thr Leu Asp Gly Gly Phe
49      50                  55                  60
51 ata tac gag gca gga ctt gcc cca tac aaa ctg cga cct gta gcg gcg   240
52 Ile Tyr Glu Ala Gly Leu Ala Pro Tyr Lys Leu Arg Pro Val Ala Ala
53  65                  70                  75                  80
55 gaa gtc tac ggg acc gaa aga caa cca cga act cac tat tat gct gtg   288
56 Glu Val Tyr Gly Thr Glu Arg Gln Pro Arg Thr His Tyr Tyr Ala Val
57              85                  90                  95
59 gct gtt gtg aag aag ggc gga tct ttt cag ctg aac gaa ctt caa ggt   336
60 Ala Val Val Lys Lys Gly Gly Ser Phe Gln Leu Asn Glu Leu Gln Gly
61              100                 105                 110
63 ctg aag tca tgc cac aca gga ctt cgc agg acc gct gga tgg aat gtc   384
64 Leu Lys Ser Cys His Thr Gly Leu Arg Arg Thr Ala Gly Trp Asn Val
65          115                 120                 125
67 cct ata ggg aca ctt cgt cca ttc ttg aat tgg acg ggt cca cct gag   432
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Input Set : A:\6184844j.app
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 68 Pro Ile Gly Thr Leu Arg Pro Phe Leu Asn Trp Thr Gly Pro Pro Glu
 69     130             135             140
 71 ccc att gag gca gct gtg gca aga ttc ttc tca gcc tct tgt gtt cca      480
 72 Pro Ile Glu Ala Ala Val Ala Arg Phe Phe Ser Ala Ser Cys Val Pro
 73 145             150             155             160
 75 ggt gca gat aaa gga caa ttc ccc aac ctt tgt cgc ctg tgt gcg ggg      528
 76 Gly Ala Asp Lys Gly Gln Phe Pro Asn Leu Cys Arg Leu Cys Ala Gly
 77             165             170             175
 79 aca ggg gaa aac aaa tgt gca ttc tca tcc cag gaa ccg tac ttc agc      576
 80 Thr Gly Glu Asn Lys Cys Ala Phe Ser Ser Gln Glu Pro Tyr Phe Ser
 81             180             185             190
 83 tac tct ggt gcc ttt aag tgt ctt aga gac ggt gct gga gat gtt gct      624
 84 Tyr Ser Gly Ala Phe Lys Cys Leu Arg Asp Gly Ala Gly Asp Val Ala
 85         195             200             205
 87 ttt att aga gag agc aca gtg ttt gag gat ctt tca gac gag gct gaa      672
 88 Phe Ile Arg Glu Ser Thr Val Phe Glu Asp Leu Ser Asp Glu Ala Glu
 89     210             215             220
 91 agg gac gag tat gag tta ctc tgc cca gac aac act cgt aag cca gtt      720
 92 Arg Asp Glu Tyr Glu Leu Leu Cys Pro Asp Asn Thr Arg Lys Pro Val
 93 225             230             235             240
 95 gac aag ttc aaa gat tgc cat ctt gca cgg gtc cct tct cat gcc gtt      768
 96 Asp Lys Phe Lys Asp Cys His Leu Ala Arg Val Pro Ser His Ala Val
 97             245             250             255
 99 gtg gca cga agt gtt aat gga aag gag gat gcc atc tgg aat ctt ctc      816
100 Val Ala Arg Ser Val Asn Gly Lys Glu Asp Ala Ile Trp Asn Leu Leu
101             260             265             270
103 cgc caa gca cag gaa aag ttt gga aag gac aag tca ccg aaa ttc cag      864
104 Arg Gln Ala Gln Glu Lys Phe Gly Lys Asp Lys Ser Pro Lys Phe Gln
105         275             280             285
107 ctc ttt ggt tcc cct agt ggg cag aaa gat ctt ctg ttc aag gac tct      912
108 Leu Phe Gly Ser Pro Ser Gly Gln Lys Asp Leu Leu Phe Lys Asp Ser
109     290             295             300
111 gcc att ggg ttt tcg aga gtg cca cct agg ata gat tct ggg ttg tac      960
112 Ala Ile Gly Phe Ser Arg Val Pro Pro Arg Ile Asp Ser Gly Leu Tyr
113 305             310             315             320
115 ctt ggc tcc gga tac ttt act gca att cag aac ttg agg aaa agt gag     1008
116 Leu Gly Ser Gly Tyr Phe Thr Ala Ile Gln Asn Leu Arg Lys Ser Glu
117             325             330             335
119 gag gaa gtt gct gcc cgg cgt gcg cgg gtc gtt tgg tgt gcg gtg gga     1056
120 Glu Glu Val Ala Ala Arg Arg Ala Arg Val Val Trp Cys Ala Val Gly
121         340             345             350
123 gag caa gag ttg cgc aag tgt aac cag tgg agt ggt ttg agc gaa gga     1104
124 Glu Gln Glu Leu Arg Lys Cys Asn Gln Trp Ser Gly Leu Ser Glu Gly
125         355             360             365
127 tct gtg acc tgc tca tcg gcc tcc act aca gaa gat tgc atc gcc ctg     1152
128 Ser Val Thr Cys Ser Ser Ala Ser Thr Thr Glu Asp Cys Ile Ala Leu
129     370             375             380
131 gtg ttg aaa gga gaa gct gat gcc atg agt ttg gat gga gga tat gtt     1200
132 Val Leu Lys Gly Glu Ala Asp Ala Met Ser Leu Asp Gly Gly Tyr Val
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133 385                  390                  395                  400
135 tac act gca ggt aaa tgt ggt ttg gtg cct gtc ctt gca gag aac tac   1248
136 Tyr Thr Ala Gly Lys Cys Gly Leu Val Pro Val Leu Ala Glu Asn Tyr
137             405                  410                  415
139 aaa tca caa caa agc agt gac cct gat cct aac tgt gtg gat aga cct   1296
140 Lys Ser Gln Gln Ser Ser Asp Pro Asp Pro Asn Cys Val Asp Arg Pro
141             420                  425                  430
143 gtg gaa gga tat ctt gct gtg gcg gtg gtt agg aga tca gac act agc   1344
144 Val Glu Gly Tyr Leu Ala Val Ala Val Val Arg Arg Ser Asp Thr Ser
145         435                  440                  445
147 ctt acc tgg aac tct gtg aaa ggc aag aag tcc tgc cac acc gcc gtg   1392
148 Leu Thr Trp Asn Ser Val Lys Gly Lys Lys Ser Cys His Thr Ala Val
149     450                  455                  460
151 gac agg act gca ggt tgg aat atc ccc atg gga ttg ctc ttc aac cag   1440
152 Asp Arg Thr Ala Gly Trp Asn Ile Pro Met Gly Leu Leu Phe Asn Gln
153 465                  470                  475                  480
155 acg ggc tcc tgc aaa ttt gat gaa tat ttc agt caa agc tgt gcc cct   1488
156 Thr Gly Ser Cys Lys Phe Asp Glu Tyr Phe Ser Gln Ser Cys Ala Pro
157             485                  490                  495
159 ggt tct gac cca aga tct aat ctc tgt gct ttg tgt att gga gat gag   1536
160 Gly Ser Asp Pro Arg Ser Asn Leu Cys Ala Leu Cys Ile Gly Asp Glu
161             500                  505                  510
163 caa ggt gag aat aag tgc gtt ccc aac agc aac gag aga tac tac ggt   1584
164 Gln Gly Glu Asn Lys Cys Val Pro Asn Ser Asn Glu Arg Tyr Tyr Gly
165         515                  520                  525
167 tac act ggg gct ttc cgt tgc ttg gct gag aat gct gga gac gtt gca   1632
168 Tyr Thr Gly Ala Phe Arg Cys Leu Ala Glu Asn Ala Gly Asp Val Ala
169     530                  535                  540
171 ttt gtg aaa gat gtc act gtc ttg cag aac act gat gga aat aac aat   1680
172 Phe Val Lys Asp Val Thr Val Leu Gln Asn Thr Asp Gly Asn Asn Asn
173 545                  550                  555                  560
175 gag gca tgg gct aag gat ttg aag ctt gca gac ttt gcg ttg ctg tgc   1728
176 Glu Ala Trp Ala Lys Asp Leu Lys Leu Ala Asp Phe Ala Leu Leu Cys
177             565                  570                  575
179 ctc gat ggc aaa cgt aag cct gtg act gaa gct aga agc tgc cat ctt   1776
180 Leu Asp Gly Lys Arg Lys Pro Val Thr Glu Ala Arg Ser Cys His Leu
181             580                  585                  590
183 gcc atg gcc ccg aat cat gct gtg gtg tct cgt atg gat aag gtg gaa   1824
184 Ala Met Ala Pro Asn His Ala Val Val Ser Arg Met Asp Lys Val Glu
185         595                  600                  605
187 cgc ttg aaa cag gtg ttg ctc cac caa cag gct aaa ttt ggt aga aat   1872
188 Arg Leu Lys Gln Val Leu Leu His Gln Gln Ala Lys Phe Gly Arg Asn
189     610                  615                  620
191 gga tct gac tgc ccg gac aag ttt tgc tta ttc cag tct gaa acc aaa   1920
192 Gly Ser Asp Cys Pro Asp Lys Phe Cys Leu Phe Gln Ser Glu Thr Lys
193 625                  630                  635                  640
195 aac ctt ttg ttc aat gac aac act gag tgt ctt gcc aga ctc cat ggc   1968
196 Asn Leu Leu Phe Asn Asp Asn Thr Glu Cys Leu Ala Arg Leu His Gly
197             645                  650                  655
```

```
199 aaa aca aca tat gaa aaa tat ttg gga cca cag tat gtc gca ggc att    2016
200 Lys Thr Thr Tyr Glu Lys Tyr Leu Gly Pro Gln Tyr Val Ala Gly Ile
201             660             665             670
203 act aat ctg aaa aag tgc tca acc tcc cca ctc cta gaa gcc tgt gaa    2064
204 Thr Asn Leu Lys Lys Cys Ser Thr Ser Pro Leu Leu Glu Ala Cys Glu
205         675             680             685
207 ttc cta agg aag taa                                                2079
208 Phe Leu Arg Lys
209     690
212 <210> SEQ ID NO: 2
213 <211> LENGTH: 30
214 <212> TYPE: DNA
215 <213> ORGANISM: Artificial Sequence
217 <220> FEATURE:
218 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
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221 ggatccatgg gccgtaggag aaggagtgtt                                   30
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225 <211> LENGTH: 32
226 <212> TYPE: DNA
227 <213> ORGANISM: Artificial Sequence
229 <220> FEATURE:
230 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
232 <400> SEQUENCE: 3
233 gagctccttc ggttttactt cctgaggaat tc                                32
236 <210> SEQ ID NO: 4
237 <211> LENGTH: 42
238 <212> TYPE: DNA
239 <213> ORGANISM: Artificial Sequence
241 <220> FEATURE:
242 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
244 <400> SEQUENCE: 4
245 tctagataaa ataatctata cattaaaaaa tttgatttta aa                     42
248 <210> SEQ ID NO: 5
249 <211> LENGTH: 36
250 <212> TYPE: DNA
251 <213> ORGANISM: Artificial Sequence
253 <220> FEATURE:
254 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
256 <400> SEQUENCE: 5
257 ggatccgact gagtcggata agaagaaaag aaaaga                            36
260 <210> SEQ ID NO: 6
261 <211> LENGTH: 36
262 <212> TYPE: DNA
263 <213> ORGANISM: Artificial Sequence
265 <220> FEATURE:
266 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
268 <400> SEQUENCE: 6
269 tctagagttt tcaaatttga attttaatgt gtgttg                            36
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PATENT APPLICATION: US/09/743,823   TIME: 14:15:45

Input Set : A:\6184844j.app
Output Set: N:\CRF3\11142001\I743823.raw

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272 <210> SEQ ID NO: 7
273 <211> LENGTH: 36
274 <212> TYPE: DNA
275 <213> ORGANISM: Artificial Sequence
277 <220> FEATURE:
278 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
280 <400> SEQUENCE: 7
281 ggatcccacc ttaaggaggt tgcaacgagc gtggca                      36
284 <210> SEQ ID NO: 8
285 <211> LENGTH: 250
286 <212> TYPE: DNA
287 <213> ORGANISM: Artificial Sequence
289 <220> FEATURE:
290 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
292 <400> SEQUENCE: 8
293 ggccgtagga gaaggagtgt tcaatggtgc gcagtatcac aaccagaggc cacaaaatgc 60
294 ttccaatggc aaaggaatat gagaaaagtt cgtggacctc ctgtatcttg cataaagaga 120
295 gattcaccca tccagtgtat ccaggcaatt gcggaaaaca gagctgatgc tgtgactctt 180
296 gatggtggtt tcatatacga ggcaggactt gccccataca aactgcgacc tgtagcggcg 240
297 gaagtctacg                                                   250
300 <210> SEQ ID NO: 9
301 <211> LENGTH: 250
302 <212> TYPE: DNA
303 <213> ORGANISM: Artificial Sequence
305 <220> FEATURE:
306 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
308 <400> SEQUENCE: 9
309 gcacctggaa cacaagaggc tgagaagaat cttgccacag ctgcctcaat gggctcaggt 60
310 ggacccgtcc aattcaagaa tggacgaagt gtccctatag ggacattcca tccagcggtc 120
311 ctgcgaagtc ctgtgtggca tgacttcaga ccttgaagtt cgttcagctg aaaagatccg 180
312 cccttcttca caacagccac agcataatag tgagttcgtg gttgtctttc ggtcccgtag 240
313 acttccgccg                                                   250
316 <210> SEQ ID NO: 10
317 <211> LENGTH: 250
318 <212> TYPE: DNA
319 <213> ORGANISM: Artificial Sequence
321 <220> FEATURE:
322 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
324 <400> SEQUENCE: 10
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326 tgaaagatcc tcaaacactg tgctctctct aataaaagca acatctccag caccgtctct 120
327 aagacactta aaggcaccag agtagctgaa gtacggttcc tgggatgaga atgcacattt 180
328 gttttcccct gtccccgcac acaggcgaca aaggttgggg aattgtcctt tatctgcacc 240
329 tggaacacaa                                                   250
332 <210> SEQ ID NO: 11
333 <211> LENGTH: 255
334 <212> TYPE: DNA
335 <213> ORGANISM: Artificial Sequence
337 <220> FEATURE:
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Use of n and / or Xaa has been detected in the
Sequence Listing. Review the Sequence Listing
to ensure a corresponding explanation is present
in the <220> to <223> fields of each sequence
using n or Xaa.

VERIFICATION SUMMARY   DATE: 11/14/2001
PATENT APPLICATION: US/09/743,823   TIME: 14:15:46

Input Set : **A:\6184844j.app**
Output Set: **N:\CRF3\11142001\I743823.raw**

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L:758 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:762 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:763 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:764 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
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